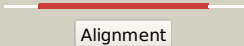
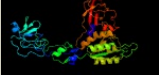
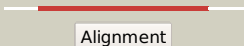

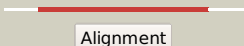




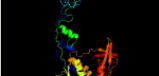

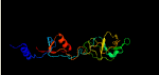
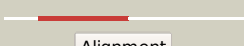
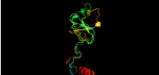

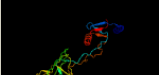

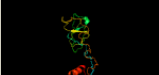















# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0994\_(moeA1)\_1110273\_1111553  
 Date Wed Jul 31 22:05:06 BST 2019  
 Unique Job ID 33ec5523090a958a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nqqA_</a>	 Alignment		100.0	30	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
2	<a href="#">c5g2rA_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein cnx1; <b>PDBTitle:</b> crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
3	<a href="#">c1uz5A_</a>	 Alignment		100.0	31	<b>PDB header:</b> molybdopterin biosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> 402aa long hypothetical molybdopterin <b>PDBTitle:</b> the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
4	<a href="#">c2fu3A_</a>	 Alignment		100.0	32	<b>PDB header:</b> biosynthetic protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin; <b>PDBTitle:</b> crystal structure of gephyrin e-domain
5	<a href="#">c1wu2B_</a>	 Alignment		100.0	27	<b>PDB header:</b> structural genomics,biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis moea protein; <b>PDBTitle:</b> crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
6	<a href="#">d1uz5a2</a>	 Alignment		100.0	31	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
7	<a href="#">d1wu2a2</a>	 Alignment		100.0	30	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
8	<a href="#">d2nqra2</a>	 Alignment		100.0	29	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
9	<a href="#">d2ftsa2</a>	 Alignment		100.0	34	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
10	<a href="#">d2nqra3</a>	 Alignment		100.0	32	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
11	<a href="#">d2ftsa3</a>	 Alignment		100.0	30	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like

12	<a href="#">d1uz5a3</a>	Alignment		100.0	38	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
13	<a href="#">d1wu2a3</a>	Alignment		100.0	24	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
14	<a href="#">c2pjkA</a>	Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 178aa long hypothetical molybdenum cofactor <b>PDBTitle:</b> structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
15	<a href="#">d1xi8a3</a>	Alignment		100.0	25	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
16	<a href="#">d1y5ea1</a>	Alignment		100.0	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
17	<a href="#">d1mkza</a>	Alignment		100.0	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
18	<a href="#">c2is8A</a>	Alignment		100.0	22	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis enzyme, moab; <b>PDBTitle:</b> crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
19	<a href="#">d1jlja</a>	Alignment		99.9	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
20	<a href="#">c2qq1A</a>	Alignment		99.9	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor biosynthesis mog; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
21	<a href="#">d2g2ca1</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
22	<a href="#">c3kbqA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein ta0487; <b>PDBTitle:</b> the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum <b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
23	<a href="#">c3rfqC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis mog protein; <b>PDBTitle:</b> anomalous substructure of moga
24	<a href="#">c2g4rB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin biosynthesis mog protein; <b>PDBTitle:</b> anomalous substructure of moga
25	<a href="#">d1uuya</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
26	<a href="#">c4lhbC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> molybdopterin adenyltransferase; <b>PDBTitle:</b> crystal structure of tungsten cofactor synthesizing protein moab from2 pyrococcus furiosus
27	<a href="#">d2f7wa1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
28	<a href="#">c4xcwF</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> molybdopterin adenyltransferase; <b>PDBTitle:</b> crystal structure of molybdenum cofactor biosynthesis protein moga2 from helicobacter pylori str. j99

29	<a href="#">c4uuwA</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> cina-like protein; <b>PDBTitle:</b> competence or damage-inducible protein cina from thermus thermophilus
30	<a href="#">d1di6a</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
31	<a href="#">d1xi8a2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> MoeA N-terminal region -like <b>Superfamily:</b> MoeA N-terminal region -like <b>Family:</b> MoeA N-terminal region -like
32	<a href="#">d2nqra1</a>	Alignment	not modelled	99.5	28	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
33	<a href="#">d2ftsA1</a>	Alignment	not modelled	99.3	27	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
34	<a href="#">d1wu2a1</a>	Alignment	not modelled	99.3	22	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
35	<a href="#">d1xi8a1</a>	Alignment	not modelled	99.2	28	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
36	<a href="#">d1uz5a1</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> beta-clip <b>Superfamily:</b> MoeA C-terminal domain-like <b>Family:</b> MoeA C-terminal domain-like
37	<a href="#">c2rirA</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
38	<a href="#">d1gpma2</a>	Alignment	not modelled	93.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
39	<a href="#">c3d4oA</a>	Alignment	not modelled	92.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
40	<a href="#">d7reqa2</a>	Alignment	not modelled	91.8	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
41	<a href="#">c3c7cB</a>	Alignment	not modelled	91.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
42	<a href="#">d1l9xa</a>	Alignment	not modelled	91.4	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
43	<a href="#">c1l9xA</a>	Alignment	not modelled	91.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> structure of gamma-glutamyl hydrolase
44	<a href="#">c2yxbA</a>	Alignment	not modelled	91.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
45	<a href="#">d1pjca1</a>	Alignment	not modelled	90.6	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
46	<a href="#">d1ccwa</a>	Alignment	not modelled	89.1	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
47	<a href="#">c3louB</a>	Alignment	not modelled	88.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
48	<a href="#">c2eezG</a>	Alignment	not modelled	88.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
49	<a href="#">d1q7ra</a>	Alignment	not modelled	88.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
50	<a href="#">c3d54D</a>	Alignment	not modelled	88.6	24	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 1; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
51	<a href="#">c3rgwS</a>	Alignment	not modelled	88.6	11	<b>PDB header:</b> oxidoreductase/oxidoreductase <b>Chain:</b> S; <b>PDB Molecule:</b> membrane-bound hydrogenase (nife) small subunit hoXk; <b>PDBTitle:</b> crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
52	<a href="#">d1t3ta2</a>	Alignment	not modelled	88.5	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
53	<a href="#">d1fmfa</a>	Alignment	not modelled	88.2	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
54	<a href="#">d1i7qb</a>	Alignment	not modelled	88.1	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
						<b>PDB header:</b> hydrolase

55	<a href="#">c6a4tB_</a>	Alignment	not modelled	87.9	13	<b>Chain:</b> B: <b>PDB Molecule:</b> peptidase e; <b>PDBTitle:</b> crystal structure of peptidase e from deinococcus radiodurans r1
56	<a href="#">c3w7bB_</a>	Alignment	not modelled	87.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
57	<a href="#">d1yq9a1</a>	Alignment	not modelled	87.4	14	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nickel-iron hydrogenase, small subunit
58	<a href="#">c3l4eA_</a>	Alignment	not modelled	86.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
59	<a href="#">c3o1lB_</a>	Alignment	not modelled	86.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
60	<a href="#">c3myrE_</a>	Alignment	not modelled	86.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> hydrogenase (nife) small subunit hyda; <b>PDBTitle:</b> crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
61	<a href="#">c4l8fA_</a>	Alignment	not modelled	86.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl hydrolase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
62	<a href="#">d1jvna2</a>	Alignment	not modelled	86.0	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
63	<a href="#">c3n0vD_</a>	Alignment	not modelled	85.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> formyltetrahydrofolate deformylase; <b>PDBTitle:</b> crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
64	<a href="#">c3en0A_</a>	Alignment	not modelled	85.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
65	<a href="#">d1ka9h_</a>	Alignment	not modelled	85.4	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
66	<a href="#">d1wuis1</a>	Alignment	not modelled	84.7	17	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nickel-iron hydrogenase, small subunit
67	<a href="#">c5mvrA_</a>	Alignment	not modelled	84.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of bacillus subtilus ydib
68	<a href="#">c6qurA_</a>	Alignment	not modelled	84.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> mapping the allosteric communication network of aminodeoxychorismate2 synthase
69	<a href="#">d1wl8a1</a>	Alignment	not modelled	84.5	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
70	<a href="#">c4gudA_</a>	Alignment	not modelled	84.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit hish; <b>PDBTitle:</b> crystal structure of amidotransferase hish from vibrio cholerae
71	<a href="#">d1l7da1</a>	Alignment	not modelled	84.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
72	<a href="#">c4ycsC_</a>	Alignment	not modelled	83.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
73	<a href="#">c6ehqT_</a>	Alignment	not modelled	83.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> hydrogenase-2 small chain; <b>PDBTitle:</b> e. coli hydrogenase-2 (as isolated form).
74	<a href="#">d2naca2</a>	Alignment	not modelled	83.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
75	<a href="#">d1l1qb_</a>	Alignment	not modelled	81.8	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
76	<a href="#">c1u4sA_</a>	Alignment	not modelled	81.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
77	<a href="#">c1np3B_</a>	Alignment	not modelled	80.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxyoxy acid isomeroreductase from2 pseudomonas aeruginosa
78	<a href="#">d2a9va1</a>	Alignment	not modelled	80.6	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
79	<a href="#">d9ldta1</a>	Alignment	not modelled	80.2	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
80	<a href="#">d1qdlb_</a>	Alignment	not modelled	80.2	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
						<b>Fold:</b> Flavodoxin-like

81	<a href="#">d1sc6a2</a>	Alignment	not modelled	80.0	11	<b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
82	<a href="#">d1lagxa</a>	Alignment	not modelled	79.1	16	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
83	<a href="#">c4hh3C</a>	Alignment	not modelled	77.0	15	<b>PDB header:</b> flavoprotein/transcription <b>Chain:</b> C: <b>PDB Molecule:</b> appa protein; <b>PDBTitle:</b> structure of the appa-pps2 core complex from rb. sphaeroides
84	<a href="#">d1frfs</a>	Alignment	not modelled	76.9	15	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nickel-iron hydrogenase, small subunit
85	<a href="#">d1k9vf</a>	Alignment	not modelled	76.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
86	<a href="#">c3fijD</a>	Alignment	not modelled	75.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> lin1909 protein; <b>PDBTitle:</b> crystal structure of a uncharacterized protein lin1909
87	<a href="#">c3p2yA</a>	Alignment	not modelled	75.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
88	<a href="#">d1zq1a2</a>	Alignment	not modelled	75.3	20	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
89	<a href="#">c2d6fA</a>	Alignment	not modelled	75.3	17	<b>PDB header:</b> ligase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit d; <b>PDBTitle:</b> crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
90	<a href="#">d4pgaa</a>	Alignment	not modelled	75.0	18	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
91	<a href="#">c3whpA</a>	Alignment	not modelled	74.9	16	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
92	<a href="#">c1h2aS</a>	Alignment	not modelled	74.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> S: <b>PDB Molecule:</b> hydrogenase; <b>PDBTitle:</b> single crystals of hydrogenase from desulfovibrio vulgaris
93	<a href="#">d1e8ca2</a>	Alignment	not modelled	74.4	15	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
94	<a href="#">c2issF</a>	Alignment	not modelled	73.8	20	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
95	<a href="#">d1vcoa1</a>	Alignment	not modelled	73.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
96	<a href="#">c4ypoB</a>	Alignment	not modelled	73.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
97	<a href="#">d1bg6a2</a>	Alignment	not modelled	73.3	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
98	<a href="#">c2wpaA</a>	Alignment	not modelled	72.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [nifese] hydrogenase, small subunit; <b>PDBTitle:</b> structure of the oxidised, as-isolated nifese hydrogenase from d.2 vulgaris hildenborough
99	<a href="#">d1uxja1</a>	Alignment	not modelled	72.5	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
100	<a href="#">c3r74B</a>	Alignment	not modelled	72.3	26	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component i; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
101	<a href="#">d1a4ia1</a>	Alignment	not modelled	71.8	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
102	<a href="#">d1cc1s</a>	Alignment	not modelled	71.7	15	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nickel-iron hydrogenase, small subunit
103	<a href="#">c2cukC</a>	Alignment	not modelled	71.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermus thermophilus hb8
104	<a href="#">c4xdzB</a>	Alignment	not modelled	70.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
105	<a href="#">c3nxE</a>	Alignment	not modelled	70.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> cytoplasmic l-asparaginase; <b>PDBTitle:</b> crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

106	<a href="#">d1i10a1</a>	Alignment	not modelled	70.2	24	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
107	<a href="#">c2p2dA_</a>	Alignment	not modelled	69.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-asparaginase i; <b>PDBTitle:</b> crystal structure and allosteric regulation of the cytoplasmic2 escherichia coli l-asparaginase i
108	<a href="#">c2lxnA_</a>	Alignment	not modelled	69.8	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit a; <b>PDBTitle:</b> solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
109	<a href="#">c4r3uD_</a>	Alignment	not modelled	69.2	27	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyisobutyryl-coa mutase small subunit; <b>PDBTitle:</b> crystal structure of 2-hydroxyisobutyryl-coa mutase
110	<a href="#">d5ldha1</a>	Alignment	not modelled	68.8	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">d1dlja3</a>	Alignment	not modelled	68.5	7	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
112	<a href="#">c6fpeE_</a>	Alignment	not modelled	68.0	20	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> atpase yjee, predicted to have essential role in cell wall <b>PDBTitle:</b> bacterial protein complex
113	<a href="#">d1o7ja_</a>	Alignment	not modelled	67.6	18	<b>Fold:</b> Glutaminase/Asparaginase <b>Superfamily:</b> Glutaminase/Asparaginase <b>Family:</b> Glutaminase/Asparaginase
114	<a href="#">d2nv0a1</a>	Alignment	not modelled	67.1	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
115	<a href="#">d3bula2</a>	Alignment	not modelled	66.7	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
116	<a href="#">c4ei8A_</a>	Alignment	not modelled	66.5	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> plasmid replication protein repx; <b>PDBTitle:</b> crystal structure of bacillus cereus tubz, apo-form
117	<a href="#">c4jgiB_</a>	Alignment	not modelled	65.7	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
118	<a href="#">c1jvnB_</a>	Alignment	not modelled	64.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
119	<a href="#">c3e7hA_</a>	Alignment	not modelled	64.8	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor
120	<a href="#">c3k13A_</a>	Alignment	not modelled	64.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydrofolate-homocysteine methyltransferase; <b>PDBTitle:</b> structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron